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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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67
1 GGFGGLGGRGKCPS
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-399-696-118
US-08-399-936-2
US-08-928-692-10
US-08-928-692-12
US-09-160-065-2
US-09-413-814-76
US-09-413-814-76
US-08-487-8268-16
US-08-487-8268-16
US-08-16-209-5
US-08-16-309-5
US-08-929-329-12
US-08-929-329-12
US-08-928-633-2
US-08-17-8448-11
US-08-963-168C-41
US-08-963-168C-41
US-08-963-317-63
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US-08-637-759B-400

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PCT-US94-07926-43

US-08-888-497-22

PCT-US94-07926-22
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                              Sequence 400, App
Sequence 43, Appl
Sequence 43, Appl
Sequence 22, Appl
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 38, Appli
Sequence 54, Appli
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Sequence 16, Appli
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Sequence 13, Appl Sequence 13, Appl	Sequence 166, App	39,	Sequence 17, Appl	10,	Sequence 44, Appl	•	•	Sequence 41, Appl	•	Sequence 45, Appl	`	Sequence 43, Appl	•	•	Sequence 40, Appl	Sequence 67, Appl	Sequence 67, Appl	Sequence 6, Appli

## ALIGNMENTS

US-08-864-038A-3

RESULT

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Sequence 3, Application US/08864038A

Patent NO. 6001592

GENERAL INFORMATION:
APPLICANT: KUNIO NAKASHIMA et al.
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES:
APPLICATION: TO SAID POLYPEPTIDE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: JP 8-184459
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. BTUCE HAMBURG
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Isshind
CITY: Tsu-city
STATE: Mie-pref
COUNTRY: JAPAN
ZIP: 514-01
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Best Local Similarity
"hes 8; Conservations
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                                                                                                        Matches
                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 400, Application US/08637759B Patent No. 5876931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                     19 SRCDGRC 25
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: David W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                     ₹37 SRCDGRC 43
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                                                                                                       Local Similarity hes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 11-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Patrea L. Pabst
2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                  : (404) ...
(404) 873-8795
TD NO: 400:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               David William Holden
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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100.0%; Pre
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                                                                                                                      10.4%; Score 7; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/GB95/02875
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Pred. No.
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; HYPOTHETICAL:
US-08-871-355A-400
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US-08-871-355A-400
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                                                                                                                                                                                                                     Patent No. 5972677
                                                                                                                                                                                                                                         Sequence 43,
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (404) 873-8795 INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                 APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisees Sequences and Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Genes NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: RP TELECOMMUNICATION INFORMATION: TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                       ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA STREET: 200 East Broward Boulevard
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
19 SRCDGRC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Georgia
                                                                                                                                                                                                                                                                                                                         37 SRCDGRC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                         Application US/08888497
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2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               David William Holden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                          Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                      10.4%; Score 7; DB 3;
100.0%; Pred. No. 1.3;
tive 0; Mismatches
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Length 47;

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Gaps

COMPUTER READABLE FORM:

33301

COUNTRY:

USA

MEDIUM TYPE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sec
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleoti
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Manso, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                            CLASSIFICATION:
                                                           APPLICATION NUMBER: PCT/
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 GLGGRG 34
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Local Similarity 100.0%; Pred. No. 35
les 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Manso, Peter J. REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/097,354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                         33301
                                                                                                                                                                                                                                                                                            Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                200 East Broward Boulevard
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                                                                                                                                                                                                                                                           USA
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US 08/097,354
                                                                                  PCT/US94/07926
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LOW Molecular Weight Amino Acid Sequences by, Antisense Sequences and Nucleotide
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US-08-888-497-22
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                                                                       INFORMATION FOR SEQ ID NO: 22
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TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                         REFERENCE/DOCKET NUMBER: IN TELECOMMUNICATION INFORMATION: 305-527-2498
                                                                                                                                                               FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MADISO, Peter J
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: IN
TELECOMMUNICATION INFORMATION:
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LENGTH: 130 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 200 East Brown CITY: Fort Lauderdale
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TOPOLOGY:
                               LENGTH:
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29 GLGGRG 34
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Local Similarity 100.0%; Pred. No. 35;
es 6; Conservative 0; Mismatches
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STRANDEDNESS: sin
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               amino acid
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                             158 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 East Broward Boulevard
                                                                                           305-764-4996
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Russell PA
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; MOLECULE TYPE: protein US-08-888-497-22
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                                      RESULT 8
US-08-399-696-4
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Sequence 4, Application US/08399696 Patent No. 5756669
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Best Local Similarity
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Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tischfield, Jay A.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: IN TELECOMMUNICATION INFORMATION: 305-527-2498
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Ruden, Barr
ADDRESSEE: Russell PA
STREET: 200 East Brows
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/097,354 FILING DATE: 26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 15-JUL-1994
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                                                                                                                       57 GLGGRG 62
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 33301
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100.0%; Pred. No. 41;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US94/07926
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, MOLECULE TYPE: protein US-08-399-696-4
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Best Local Similarity
"hes 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 118, Application US/08399696 Patent No. 5756669 GENERAL INFORMATION:
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                                   REFERENCE/DOCKET NUMBER: 15522-000710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 118:
                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/156,671
FILING DATE: 22-NOV-193
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,671
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,696
FILING DATE: 02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 GGLGGR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Smith, William REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 02-MAR
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Gaps

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-730-953-2
                                      RESULT 11
US-08-928-692-10
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Sequence 10, Application US/08928692
                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)638-4810 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE P 39
FILING DATE: 21-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
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FILING DATE: 19910723
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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nes 6; Conserv
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STRANDEDNESS: un)
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20005-5701
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655 Fifteenth Street N.W.
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100.0%; Pred. No.
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                 DB 1;
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US-08-030-096-2; Sequence 2, Application US/08030096; Patent No. 5426041
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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           COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                  APPLICANT: Fabijanski, Steven F.
APPLICANT: Arnison, Paul G.
TITLE OF INVENTION: BINARY CRYPTOCYTOTOXIC METHOD OF HYBRID
TITLE OF INVENTION: SEED PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
CURRENT APPLICATION DATA:
                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lamsa, Micha
APPLICANT: Hansen, Kim
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                                                                                                                                                          ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                    441 LGGRGK 446
                                                                                                   COUNTRY: USA
ZIP: 20007-5109
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TENERAX: 212-878-9655
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STATE: NY
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                                                                                                                                         Washington, D.C.
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                                                                                                                                                     E: Foley & Lardner 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 amino acids
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100.0%; Pred. No. 1.:
tive 0; Mismatches
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o. 1.1e+02;
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US-09-413-814-89
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; LENGTH: 568
; TYPE: PRT
; ORGANISM: Avian leukosis virus
US-09-160-065-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-030-096-2
Sequence 89, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANF: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Applicat Patent No. 6146641 GENERAL INFORMATION:
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Best Local
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APPLICANT: Hunt, Henry
TITLE OF INVENTION: Avian Leukosis Virus Subgroup J Envelope Gene Product
TITLE OF INVENTION: for Diagnosis and Vaccine
FILE REFERENCE: Docket No. 6146641 0155.98 - Lee, Lucy
CURRENT APPLICATION NUMBER: US/09/160,065
CURRENT FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lee, Lucy
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENTY Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/556,917
FILING DATE: 20-JUL-1990
PRIOR APPLICATION NUMBER: PCT/CA91/0025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                        508 FGGLGG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Product 9.0%; Score 6; DB 1; Le Local Similarity 100.0%; Pred. No. 1.1e+02; les 6; Conservative 0. Micmotal.
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100.0%; Pred. No. 1.
tive 0; Mismatches
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o. 1.2e+02
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CORRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 89
LENGTH: 590
TYPE: PRT
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                                                                                                                                                                                                      ; ORGANISM: Sorangium cellulosum US-09-413-814-76
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APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
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                                                                                                                                                                                                                                                                                             SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 76, Application US/09413814 Patent No. 6225064
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                                                                                       Matches
                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Cougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or TITLE OF INVENTION: heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535 CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1999-10-07 EARLIER FILING DATE: 1999-10-07 EARLIER FILING DATE: 1998-10-09 EARLIER FILING DATE: 1998-10-09 UNMBER: OE 198 46 493.2 EARLIER FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 107
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APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
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146 VCVPRS 151
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                                             59 VCVPRS 64
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                                                                                                               100.0%;
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
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; Pred. No.
                                                                                           Mismatches
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1.3e+02;
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US-08-460-309-5
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; FRAGMENT TYPE: N-terminal
US-08-487-826B-16
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                                                                                                                               Sequence 5, Application US/08460309 Patent No. 5837496
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                          GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                               TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                1684 NVVPKP 1689
                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sim, ...... Chetan APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                               31 NVVPKP 36
 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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Wellems, Thomas E.
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Campbell and Flores
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L00.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08125077 Patent No. 5872231 Patent No. 5872231 5840863 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1528 CVCRLG 1533
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
                                                                                                                                                                                                                                                       APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/472,319

PRILICATION NUMBER: 30-JAN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/919,951

FILING DATE: 27-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                 CITY: San Diego
STATE: California
                                                                                                            ZIP: 92122
                                                                                                                              COUNTRY:
                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 CVCRLG 51
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 22-SE
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FILING DATE: 21-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/460,309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4370 La
CITY: San Diego
STATE: Californi
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                                                                                                                                                                                 E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
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                                                                                                                              USA
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(619) 535-8949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.0%; Score 6;
100.0%; Pred. No.
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o. 5.3e+02;
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APPLICATION NUMBER: US/08/125,077 FILING DATE: 22-SEP-1993

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TOPOLOGY: US-08-125-077-5
                  US-08-929-329-12
Sequence 12, Application US/08929329; Patent No. 6120770; GENERAL INFORMATION:
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                                                                                             RESULT
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CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Patent No. 6025328
                                                                                                                                                                                                                                         Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MCMOIRIS, Trevor C. APPLICANT: Kelner, Michael J. TITLE OF INVENTION: Antitumor agents FILE REFERENCE: 103.008US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1528 CVCRLG 1533
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LENGTH: 3075 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 5
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APPLICANT: Adams, John H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 CVCRLG 51
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Local Similarity 100.0%; Pred. No. 5.3e+02;
hes 6; Conservative 0; Mismatches 0; Indels
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o. 1.4e+05;
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: 1
US-08-929-329-12
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Best Local Similarity
"~+~hes 5; Conserva
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                                               SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                              APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
                                                         CURRENT APPLICATION NUMBER: US/09/128,450
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
               LENGTH: 8
TYPE: PRT
ORGANISM: Hamster sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing TITLE OF INVENTION: Vaccine Compositions
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
ANAME: Breen, John P
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
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APPLICANT: Kappe, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: un
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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5. 1.4e+05;
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                                                                                   Query Match
Best Local Similarity
                                                                      Matches
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Patent No. 5728810
GENERAL INFORMATION:
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Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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STREET: Falls Church
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFONMUNICATION INFORMATION: TELEFHONE: (703) 205-8000 TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lewis, Randolph V. APPLICANT: Xu, Ming APPLICANT: Hinman, Michael B.
                                                                                                                                                                         LOCATION: 1.9
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-APR-1995
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-106P
                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/425,069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murphy Jr., Gerald M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
4 GGLGG
                                   4 GGLGG 8
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301 No. 5728810th Washington Street
                                                                      Conservative
                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                   7.5%;
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                                                                                                                                                                           repeats."
                                                                                                                                                                                          /label= 1st_segment
/note= "first segment of spider silk protein
                                                                   0;
                                                                                   Score 5; DB 1;
Pred. No. 1.4e
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                                                                    Mismatches
                                                                   .4e+05;
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RESULT

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RESULT 24
US-08-963-168C-41
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                                                                                                                            Sequence 41, Application US/08963168C Patent No. 6127166 GENERAL INFORMATION:
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COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
TELEPHONE: (703) 241-13100
TELEPHONE: (703) 241-13100
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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APPLICANT: Lewis, Ra
APPLICANT: Xu, Ming
APPLICANT: Hinman, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
APPLICANT: Bayley, Hagan
APPLICANT: Cao, Quiping
APPLICANT: Wang, Yunjaun
TITLE OF INVENTION: MOLLUSCAN LIGAMENT POLYPEPTIDES
TITLE OF INVENTION: AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                  Local Similarity hes 5; Conserv
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                      4 GGLGG
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TELEX: 248345
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CITY: Falls Church
STATE: Virginia
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= lst_segment
/note= "first segment of spider silk protein
repeats."
                                                                                                                                                                                                                                                                                                                                                  7.5%; Score 5; DB 100.0%; Pred. No. 1..
                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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. 1.4e+05;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

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В
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US-08-963-168C-42
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MEDIJIM TYPE: BM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,168C
FILING DATE: 03-NOV-1997
ATTORNEY/ACENT INFORMATION:
NAME: Fasse, Peter J.
NAME
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Best Local Similarity
Matches 5; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 079
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
                                                         APPLICATION NUMBER: US/08/963,168C FILING DATE: 03-NOV-1997 ATTORNEY/AGENT INFORMATION: NAME: Fasse, Peter J.
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LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson P.C.
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APPLICANT: Cao, Quiping
APPLICANT: Wang, Yunjaun
TITLE OF INVENTION: MOLLUSCAN LIGAMENT POLYPEPTIDES
TITLE OF INVENTION: AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 43
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STREET: 2-
STREET: 4A
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STREET: 225 Franklin Street
CITY: Boston
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                      NAME: Fasse, Peter J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 9...9
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INFO. 1., Peter J. 32,983
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100.0%; Pr
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Search completed: July 12, 2001, 06:17:06 Job time: 22 sec
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                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 07917/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
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TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617/542-500 TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                   LOCATION: 3...3
OTHER INFORMATION:
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)GY: linear
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                                                                                                                                        7.5%; Score 5; DB 4; Le
100.0%; Pred. No. 1.4e+05;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                   Xaa = any amino acid
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                                                                                                                                           0; Indels
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                       Post-processing: Listing first 50 summaries
                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                  SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
      4:
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67
1 GGFGGLGGRGKCPSNEIFSR.....CRLGYLRNKKKVCVPRSKCG 67
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                                                                                                                                                                                                                                                                                                                                                                        425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                  OLIGO Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                           sp_organelle:*
sp_phage:*
                                                                                                        sp_mammal:*
sp_mhc:*
                                                                                                                                                   sp_fungi:*
sp_human:*
                                                                                                                                     sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Query Match Length	BB	ID	Description	lon
, 1	ο &	11.9	113	5 07	Q9V5U5	Q9v5u5 dr	drosophila
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س ح	xo ox	11.9	738	лυ	002402		
4.10	<b>co</b> co	11.9	904 922	տ ս	0/62/1	0/62/1 my 044367 my	mytilus edu mytilus edu
6	œ	11.9	1329	N	006810		
7	7	10.4	100	10	Q9SD66	9	arabidopsis
8	7	10.4	107	10	Q9LEP7	Q91ep7 b	brassica na
9	7	10.4	284	S	Q21073	Q21073 ca	caenorhabdi
10	7	10.4	313	ഗ	Q9NL74	Q9n174 le	leishmania
11	7	10.4	314	5	076140	076140 tr	trypanosoma
12	7	10.4	438	N	Q9RY66	Q9ry66 de	deinococcus
13	7	10.4	450	Ν	083238		treponema p
14	7	10.4	463	N	Q10787	Q10787 my	mycobacteri
15	7	10.4	465	2	050943	050943 bo	borrelia bu
16	7	10.4	556	N	Q9L8K4	Q918k4 my	mycobacteri
17	7	10.4	620	10	Q9FU14	Q9fu14 o	oryza sativ
18	7	10.4	652	N	068071	068071 rh	rhodobacter
19	7	10.4	682	л	022537		rhahdi.

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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4000
Q9KHF2 Q9KHF1 Q9KHF1 Q9KHF0 083335 058565 016936 016936 09ZVVO 09	
	homo sapie treponema treponema treponema

## ALIGNMENTS

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RESULT
OZAGOO
ID 22600
AC OZAGOO
ACO
        RESULT
002402
ID 00
AC 00
DT 00
DT 00
DT 00
DT 01
DE II
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185(2000).
DR EMBL; AE003826; AAF58702.1;
EMBL; AE003826; AAF58702.1;
SQ SEQUENCE 113 AA; 11288 MW; 786171CE3C6APOA3 CDC4.
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Best Local
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
GLYCINE-RICH PROTEIN.
                              01.JUL-1997 (TrEMBLrel.
01.JUL-1997 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                002402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF027686; AAB82000.1; -. Mendel; 25262; Onovi;343;25262. SEQUENCE 151 AA; 14641 MW; 3B391AC9C51087E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onobrychis viciifolia (Common sainfoin).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
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                                                                                                                                               002402
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INSOLUBLE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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044367;
01-JUN-1998
01-JUN-1998
01-OCT-2000
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01-NOV-1998
01-NOV-1998
01-JUN-2000
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Sudo S., Fujikawa T., Nagakura T.,
Nakashima K., Takahashi T.;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDIINE-9839576; PubMed-9724735;
Qin X.X., Waite J.H.;
"A potential mediator of collagen
"A potential mediator of collagen
mussel byssal threads.";
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                              Eukaryota; Metazoa; Mollusca; Mytiloidea; Mytilidae; Mytilidae; Mytilu;
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                                                                                                                                                                                                                                                                                                                                                                                                                Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structures of mollusc shell framework proteins.";
Nature 387:563-564(1997).
EMBL: D86074; BAA20466-1;
SEQUENCE 738 AA; 61723 MW; FDF984139BF3BA59 CR
SEQUENCE FROM N.A
                                                  Mytilus edulis (Blue mussel).
                                                              PRECOL-D.
                                                                        PRECOLLAGEN
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                    NCBI_TaxID=6550;
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(TTEMBLrel. 08, Last sequence update)
(TTEMBLrel. 14, Last annotation update)
BYSSAL PRECURSOR.
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100.0%; Pr
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                               Mytilus
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Last sequence update)
Last annotation update)
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Pred. No.
                                          Bivalvia;
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                                         Pteriomorphia; Mytiloida;
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Best Local S
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Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J. Taylor K., Whitehead S., Barrell B.G., The Connormal Control of Connormal Control of Connormal Control of Connormal Control of Connormal Connormal Control of Connormal Control of Connormal Control of Connormal Connormal Control of Connormal Control of Connormal Control of Connormal Connormal Control of Connormal Co
       Q9SD66
                                                                                         1318 GGFGGLGG
                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 1329 AA;
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Prodom; PD001223; -; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                            InterPro; IPR000084; -.
InterPro; IPR002173; -.
InterPro; IPR003536; -.
Pfam; PF00934; PE; 1.
                                                                                                                                                                                                                                                                                                                                                                                          "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.", Nature 393:537-544(1998).

EMBL; Z95844; CAB09271.1; ...
Tuberculist; RV1450c; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TIEMBLIFEL 04, Created)
01-JUL-1997 (TIEMBLIFEL 04, Last sequence up
01-MAR-2001 (TIEMBLIFEL 16, Last annotation
HYPOTHETICAL 107.4 KDA PROTEIN.
PGRS. FAMILY OR RV1450C OR MTCY493.04.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98070444; PubMed=9405478; Qin X.X., Coyne K.J., Waite J.H.; "Tough tendons. Mussel byssus has collagen with silk-like domains."; J. Biol. Chem. 272:32623-32627(1997).
EMBL; AF029249; AAB96638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales;
NCBI_TaxID=1773;
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Pfam; PF01391; Collagen; 7.
SEQUENCE 922 AA; 80306 MW;
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SEQUENCE
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01-MAY-2000
01-MAY-2000
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Bowers N.L., Trick M.;
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PRELIMINARY;
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"Microsynteny at the FCA region between Arabidopsis thaliana Brassica napus.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ293726; CAC01931.1; -.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Magnoliophyta; eudicotyledons; core euc Brassicales; Brassicaceae; Brassica.
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Submitted (JAN-2000) to the EM
EMBL; AL133292; CAB61953.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUTATIVE GLYCINE-RICH PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choisne N., Robert C., Brottier P., Wincker P., Cattolico Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Len Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL 10.5 KDA PROTEIN.
                                                                                                                                                                                                                                                                                     PS00095; C5_MTASE_2;
107 AA; 9714 MW;
                                                                                                                                                                                10.4%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10530 MW;
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100.0%;
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Pred.
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0; Mismatches
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                                                                                                                                                                                                                                                                                     UNKNOWN_1.
0A7BE4A01B09B1B3
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284 AA
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No.
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dicots; Rosidae; eurosids II;
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Best Local
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          Query Match
Best Local &imilarity
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Wattson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2. 2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q21073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditidae;
                                                                                                                               Gao G., Nara T., N-Shimada J., Aoki T.;
"Novel organization and sequences of five genes encoding all six enzymes for de novo pyrimidine biosynthesis in Trypanosoma cruzi.'
J. Mol. Biol. 285:149-161(1999).
                                                                                                                                                                                                                                                                                     01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
EMBL; Z68750; CAA92963.1;
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                                                                                                                                                                                                                                                                        DIHYDROOROTATE DEHYDROGENASE
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                                               SEQUENCE
                                                                                                          EMBL; AB029444; BAA94299.1; InterPro; IPR000408; -.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=31284;
                                                                                                                                                                                                                                   Leishmania mexicana amazonensis.
Eukaryota; Euglenozoa; Kinetopla
                                                                                                                                                                                                                                    Eukaryota;
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                                                             PROSITE;
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                                                                       Pro; IPR003009; PF01180; DHOdel
                                            F01180; DHOdehase; 1; PS00626; RCC1_2; Using 313 AA; 33697 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                               IPR001295; -
                                                                                                                                                                                                                                                                                  ) (TrEMBLrel.) (TrEMBLrel.
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10.4%;
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                                               ; 1.
; UNKNOWN_1
7 MW; EB75
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Last sequence update)
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Score 7
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                                                EB7558522D1E8E0A CRC64;
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7; J
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14;
 DB 5;
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            Length 313;
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076140;
01-NOV-1998
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                                                                                                                                                                   01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                   Q9RY66;
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Novel organization and sequences of five genes encoding all six enzymes for de novo pyrimidine biosynthesis in Trypanosoma cruzi.";
J. Mol. Biol. 285:149-161(1999).
EMBL; AB010286: BAA31360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gao G., Nara T., Nakajima-Shimada J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma cruzi.
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White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-TULAHUEN;
                                                                                                                       Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
                                                                                                                                                        GTP-BINDING
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pyrimidine-genes in Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                              MEDLINE=20036896; PubMed=10567266;
                                                                                                                                              DR0084
                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                          SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                    218 GFGGLGG
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7; Conserv
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AA; 34052 MW;
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Last annotation updat
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Last annotation updat
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RESULT
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Best Local
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PROSITE; PS00095; C5_MTASE_2; UNKNOWN_1.

PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.

PROSITE; PS00756; SECY_2; UNKNOWN_1.

SEQUENCE 450 AA; 50265 MW; 892BF3217F3E6E7E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O83238 PRELIMINARY: PRT; 45
083238;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequer
01-OCT-2000 (TrEMBLrel. 15, Last annote
PREPROTEIN TRANSLOCASE SUBUNIT (SECY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001203; AAC65198.1; -. TIGR; TP0208; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NICHOLS; MEDLLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01018; GTP1_OBG; 1.
PRINTS; PR00326; GTP1OBG.
ProDom; PD003114; -: 1.
PROSITE; PS00905; GTP1_OBG; 1.
SEQUENCE 438 AA; 47836 MW;
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                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002208;
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Pfam; PF01018; GTP1_OBC
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Science 286:1571-1577(1999).
EMBL; AE001871; AAF09676.1;
427 GLGGRGK 433
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                                               5 GLGGRGK 11
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                                                                                               Conservative
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100.0%; Pr
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Last annotation updat
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Best Local
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050943;
01-JUN-1998
01-JUN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Sna
                                                                                                                                                      Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson P. van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B. "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.":
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 49.1 KDA PROTEIN CY48.28C.
RV1537 OR MICY48.28C.
Mycobacterium ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q10787;
Q10787;
01-NOV-1996
                                                                              Hypothetical protein; Plasmid. SEQUENCE 465 AA; 52773 MW;
                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete). Plasmid 1p54.
                                                                                                              TIGR;
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                                                                                                                      EMBL; AE000790; AAC66282.1; -.
                                                                                                                                      Nature 390:580-586(1997).
                                                                                                                                                     burgdorferi
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=139
                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL
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NCBI_TaxID=1773;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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8 (TrEMBLrel. 06, Last s
8 (TrEMBLrel. 08, Last s
AL 52.8 KDA PROTEIN.
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          Score 7; DB 2; Pred. No. 21; 0; Mismatches
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Last annotation updat
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Matches 7; Conserv
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01-OCT-2000
01-MAR-2001
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"A Mycobacterial Protein of the Repetitive Glycine-Rich PE-PGRS Family Is Required for Macrophage Replication and Contributes to Virulence."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF201882; AAF65169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, PUTATIVE RECEPTOR KINASE.
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InterPro; IPR0001412; -.
Pfam; PF00934; PE; 1.
ProDom; PD001223; -; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
SEQUENCE 556 AA; 54576 MW; 8C8129B5D368A634 CRC64;
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                                                                                                                                                               clone:P0698G03.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AP002747; BAB17332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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                                                                                                                       Receptor; Kinase. SEQUENCE 620 AF
                                                                                                                                                                                                                             STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
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Mycobacteriaceae; Mycobacterium.
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25;
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Best Local Similarity
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Q22537;
Q1-NOV-1996 (TIEMBLICEL.
Q1-NOV-1996 (TIEMBLICEL.
Q1-NOV-1998 (TIEMBLICEL.
SIMILARITY TO COLLAGEN.
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01-AUG-1998 (TrEMBLrel. 07, Create
01-AUG-1998 (TrEMBLrel. 07, Last s
01-MAR-2001 (TrEMBLrel. 16, Last a
DNA GYRASE SUBUNIT B (EC 5.99.1.3)
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Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
-i- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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                                                                                                     Eukaryota; Metazoa;
Rhabditidae; Pelode
NCBI_TaxID=6239;
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proDom; pD149633; -; 1.
pROSITE; pS00177; TOPOISOMERASE_II;
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                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
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SEQUENCE 6
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6 (TrEMBLrel.
8 (TrEMBLrel.
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   Bacteria;
          Treponema
                                         01-NOV-1998
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                                                                                 087472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Favello A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U42841; AAC48170.1; -.
SEQUENCE 682 AA; 72150 MW; 73933507D23E98A2 CRC64;
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                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
CDNA: FL721963 FIS, CLONE HEP05583.
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  pallidum (subsp.
Spirochaetales;
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Best Local :
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007894;
01-JUL-1997 (TrEMBLrel. 04, C
01-JUL-1997 (TrEMBLrel. 04, L
01-MAY-2000 (TrEMBLrel. 13, L
MAJOR OUTER SHEATH PROTEIN HO
MSP OR TP0621.
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083337;
01-NOV-1998
01-NOV-1998
01-MAY-2000
Treponema pallidum.
Bacteria; Spirochaetales;
NCBI_TaxID=160;
[1]
                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of T spirochete."; Science 281:375-388(1998).
EMBL; AB001211; AAC65301.1; -.
TIGR; TP0317; -.
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Bacteria; Spirochaetales;
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                               Spirochaetaceae; Treponema
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TIGR; TP0621; -.
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"Intrastrain Heterogeneity of the TprK Protein of the Treponema Pallidum Nichols Strain and Street Strain 14.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF261075; AAF76884.1; -.
SEQUENCE 758 AA; 81334 MW; DF91F1ED0F6CB3D7 CRC64;
                                                                                                                                                                                                                                                                                                               Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
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Bacteria; Spirochaetales; Spirochaetaceae; Treponema
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

B Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Nather S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.

A Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";

Nature 393:537-544(1998).

RINGERMATTY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGRS
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                                                                                          "Cloning of a yeast U1 snRNP 70K protein homologue: functional conservation of an RNA-binding domain between humans and yeast EMBO J. 10:2627-2634(1991).
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MEDLINE-91330888; PubMed-1714384;
Smith V., Barrell B.G.;
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS ASSOCIATED WITH SN-RNP U1. IT BIND STEM LOOP I OF U1 SNRNA.
MEDLINE=94039112; PubMed=8223615; Wagner P., Grimaldi M., Jenkins J.R.; "Putative dehydrogenase tms1 suppresses p53 tumour mutant in fission yeast."; Eur. J. Biochem. 217:731-736(1993).
                                                                                                                                                                                                                                                                                                                                01-UN-1994 (Rel. 29, Created)
01-CT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
PUTATIVE SORBITOL DEHYDROGENASE (EC 1.1.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000504; -.

Pfam; PF00076; rrm; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM_RNP_1; 1.

Nuclear protein; Ribonucleoprotein; RNA-binding.

DOMAIN 107 198 RNA-BINDING (RRM).
                                                                                                                                            Lyne M., Rajandream M.A., Barrell B.G., Beck A., Borzym K., Langer I., Reinhardt R.;
                                                                                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetalese;
                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                     2-DEHYDROGENASE) (TMS1 PROTEIN).
TMS1 OR SPC1773.05C.
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PIR; S48418; S48418.
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EMBL; X59986; CAA42602.1;
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                                                                                                                               Submitted
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Schizosaccharomyces.
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NSFAC; T01242; -.
; S0001323; SNP1.
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0; Mismatches
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Best Local
                                                                                                                                                                                                 ROBISON K., SMITH D.R.;
SUBMITTED (MAR-1994) TO THE EMBL/GenBank/DDBJ databases.

-i- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH
THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).

-i- COPACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- SUBCELLULAR LOCATIONS TO THE DNAJ FAMILY.

-i- SIMILARITY: BELONGS TO THE DNAJ FAMILY.

-i- SIMILARITY: CONTAINS 1 CR DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNAJ2 OR B1937_F2_56.
Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (Rel. 40, Cr
01-OCT-2000 (Rel. 40, La
01-OCT-2000 (Rel. 40, La
CHAPERONE PROTEIN DNAJ2.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Corynebacterineae;
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een the Swiss Institute of Bioinformatics and the EN
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PS00059; ADH_ZINC;
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005825;
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01-OCT-2000 (Rel. 40, Las
01-OCT-2000 (Rel. 40, Las
CHAPERONE PROTEIN DNAJ2.
                                                                                                                     MEDLINE-98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Davies R., Davies K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E. Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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Nature 393:537-544(1998).
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PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                  FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).

COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).
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CYTOPLASMIC
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(BY SIMI
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o. 3.7;
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pfam; PF00684; DnaJ_C; 1.
pfam; PF01556; DnaJ_C; 1.
prINTS; PR00625; DNAJPROTEIN.
                                    SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                          Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                  FFH OR MPN061 OR MP093.
                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-
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P75054;
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HSSP; P25685;
               Herrmann R.;
                                                                                                Mycoplasmataceae; Mycoplasma
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 Complets sequence analysis of the genome of the
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PS00637;
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P35527; Q14665;
01-JUN-1994 (Rel.
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Nucleic Acids Res. 24:4420-4449(1996).
Nucleic Acids Res. 24:4420-4449(1996).
PROTEION: NECESSARY FOR EFFICIENT EXPORT OF
PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN
RIBOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformative including as its concern use by non-profit institutions as long as its concern use by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
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                                                                                                                                                                                                                                Homo sapiens (Human).
Homo sapiens (Human).
harvota; Metazoa; Chordata;
harvata; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prosite; PS00300; SRP54; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                       TISSUE=Foot sole tissue; MEDLINE=94131202; PubMed=7507869; MEDLINE=94131202; PubMed=7507869; Melandpein L., Heid H.W., Moll I., Franke "Molecular characterization of the body cytokeratin 9: cDNA cloning, amino acid specificity of gene expression."; Differentiation 55:57-72(1993).
                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Last se
15-JUL-1998 (Rel. 36, Last an
KERATIN, TYPE I CYTOSKELETAL
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                                                  SEQUENCE OF 449-465.
MEDLINE=90267446; PubMed=2140676;
Rosen E.M., Meromsky L., Romero R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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VARIANTS
                         Biochem.
                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                        "Human
                                                                                                                                                                                                                                                                                                                                                                                                                                   441 GFGGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GFGGLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS
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EPPK LYS-160;
                          Biophys.
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                          Res.
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293
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192
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, Last annotation |
SKELETAL 9 (CYTOKE
                                                                                                                                                                                                                                                                                                                                        Created)
                          Commun.
GLN-162 AND TRP-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , WM
                                     mero R., Setter E., Goldberg I
epithelial scatter protein.";
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0; Mismatches
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M-DOMAIN:
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                            168:1082-1088(1990).
                                                                                                                                                                                                                                                                                               otation update)
(CYTOKERATIN 9) (K9) (CK 9).
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                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                              Franke W.W.;
                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                     622
                                                                                                                                  site-specific human epidermal sequence, and tissue
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SARANA ARANA ARANA BARANA BARA
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                                                                                                                                                                                                                                                                                                                                                                                                     Disease
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MIM; 144200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X75015; CAA52924.1; -. EMBL; Z29074; CAA82315.1; -. EMBL; S69510; AAC60619.1; -. PIR; B35494; B35494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hohl D., Roop D.R.;

"Mutations in the la domain of keratin 9 in patients epidermolytic palmoplantar keratoderma.";

J. Invest. Dermatol. 104:430-433(1995)

-I- FUNCTION: MAY SERVE AN IMPORTANT SPECIAL FUNCTION MATURE PALMAR AND PLANTAR SKIN TISSUE OR IN THE
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001664; -. InterPro; IPR002957; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00226; IF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothnagel J.A., Wojcik S., Liefer K.M., Dominey A.M., Huber M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS EPPK
                                                                                                                                                                                                                                                                                                                                                                                                                             Intermediate
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(EPPK).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dreschler M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLACENTAL SCATTER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P02876; 2WGC.
                                                                                                                                                                                                                                                                                                                                                                                                       mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hennies H.-C
      622 AA;
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                              12
                                                                                                                                                                                                                                                                                                                                                                                                                        filament;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       filament;
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PubMed=7532199;
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460
622
187
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298
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      61987 MW;
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                                                              N -> K (IN EPPK).
/FIId=VAR_003822.
R -> Q (IN EPPK).
/FIId=VAR_003823.
R -> W (IN EPPK).
/FIId=VAR_00384.
                                                                                                                                                                                                                                                                                             TAIL.
COIL 1A.
LINKER 1.
/FTId=VAR_003825.
T -> SR (IN CAA82315).
; 898C3825D4B5ED94 CRC64;
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LINKER 12.
                                                                                                                                                                                                               POLY-GLY
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Best Local Similarity
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Matches 7
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P01498;
21-JUL-1986 (Rel. C
21-JUL-1986 (Rel. C
01-NOV-1995 (Rel. 3
NEUROTOXIN P2.
                EMBO
                                                                                                                                        TMC3_OENBE STANDARD; PRT; 79 AA. P08747; 01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) HYPOTHETICAL 9.2 KDA PROTEIN IN COXIII REGION.
                                                                                                                                                                                                                                                                                                                                       DISULFID DISULFID
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                 mitochondria are transcribed EMBO J. 6:29-34(1987).
                                   "The cytochrome oxidase subunit
                                                      STRAIN-CV.
                                                                                             Myrtales; Onagraceae;
                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                         Mitochondrion.
                                                                                                                                   Oenothera bertiana
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                                                                SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=3950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Androctonus mauretanicus mauretanicus (Scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Androctonus.
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                PIR; A01758; NTSRPM.
                                                                                                                                                                                                                                                                                                                                                                                                        Toxicon 23:113-125(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                             toxic to
                                                                                                                                                                                                                                                                                                                                                                                                                                    scorpion
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosso J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=85193276; PubMed=3992595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6860;
                                                                                                                                                                                                                                                                                                                                                                             Neurotoxin
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       MISCELLANEOUS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Androctonus mauretanicus
                                                                                                                                                                                                                                                                                                                                                                                                                             the mouse."
                                                       MUNZIA;
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01, Last sequence 32, Last annotations
       POSITION 54 IS
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213E69262289EB5A CRC64;
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                          ter W., Brennicke A.;
nit I and subunit III
from identical promo
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Pred. No.
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       MODIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                    from the venom of the Moroccan mauretanicus, six of which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                   primrose).
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                                                                                                                                                                                                                                                                                       DB 1;
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       ВҮ
                          promoter sequences.";
       RNA EDITING
                                                                                                                                                                                                                                                                                                Length 35;
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RESULT 12
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Matches 6
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Wuchereria.
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RL3_PLARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ragahavan N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scott A.L., Josh S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRAZIL;
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01-NOV-1997 (Rel. 35, La
30-MAY-2000 (Rel. 39, La
50c RIBOSOMAL PROTEIN L
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P39878;
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MEDLINE-94364995; PubMed-8083202; Chen J., Engle S.J., Seilhamer J.J., Tischfield J.A.; Chen J., Engle S.J., Seilhamer J.J., Tischfield J.A.; "Cloning and characterization of novel rat and mouse low molecular "Cloning and characterization of novel rat and mouse low molecular "Cloning and characterization of novel rat and mouse low molecular "Cloning and characterization of novel rat and mouse low molecular "J. Biol. Chem. 269:23018-23024(1994).
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Donadio S.
                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
14 KDA PHOSPHOLIPASE A2 PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
2-ACYLHYDROLASE) (PLA2-8) (GROUP IIC PHOSPHOLIPASE A2).
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NON_TER 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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PROSITE; PS00474; RIBOSOMAL_L3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                   Craniata; Ver
Sciurognathi;
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Streptosporangiaceae;
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thi; Muridae; Murinae; Rat
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01-NOV-1997
01-NOV-1997
STRAIN-AM1 / NCIB 9133;

MEDIINE-94292425; pubmed-8021187;

Chistoserdov A.Y., Chistoserdova L.V., McIntire W.S., Lidstrom M.E.;

"Genetic organization of the mau gene cluster in Methylobacterium extorquens AM1: complete nucleotide sequence and generation and characteristics of mau mutants.";

J. Bacteriol. 176:4052-4065(1994).

-!- FUNCTION: INVOLVED IN ELECTRON TRANSFER (POTENTIAL).

-!- PATHMAY: METRILAMINE UTILIZATION.

-!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID DISULFID DISULFID DISULFID DISULFID
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PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I'- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2 ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
-I- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLLINE + H(2)O = 1-ACYLGLYCERYL-PHOSPHOCHOLINE + A FATTY ACID ANION.
-I- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. MAY REPRESENT A NEW SUBTYPE OF GROUP II PLA2.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=408;
                                                                                                                                                                                                                                                                                                                                                                                                                       Methylobacterium group; Methylobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylobacterium extorquens.
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Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                             Unpublished observations (JUN-1996).
--- SIMILARITY: BELONGS TO THE SSP FAMILY OF RIBOSOMAL PROTEINS:
--- CAUTION: THIS IS A CONCEPTUAL TRANSLATION, A FRAMESHIFT WAS
INTRODUCED IN POSITION 24 TO MODIFY THE N-TERMINUS SO AS TO
MAXIMIZE THE SIMILARITY WITH OTHER MEMBERS OF THIS FAMILY.
                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                           PROSITE; PS00585; RIBOSOMAL_S5; 1.
                                                                                                                          EMBL; M20632; AAA40074.1;
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                                                                                                                                                                                                                                                                                                                                                                          CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                    Heller D.L., Gianola K.M., Leinwand "A highly conserved mouse gene with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=88302198; PubMed=3405219;
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Mammalia; Eutheria; Rodentia;
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-1- SIMILARITY: BELONGS TO THE SURE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                        MGI:105110; Llrep3.
                                                                                                          A31139; A31139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCRLGY 177
                                                                                                                                                                                                                                                                                                                                                                                                       Cell. Biol. 8:2797-2803(1988).
                                              PF00333; Ribosomal_S5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01975;
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                protein;
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31217 MW;
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100.0%; Pr
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Pred. No.
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 90E5DB564AA624CC CRC64;
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034136;
15-JUL-1998
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of rat ribosomal protein S2. A ribosomal protein with arginine-glycine tandem repeats and RGGF motifs that are associated with nucleolar localization and binding to ribonucleic
                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P27952;
01-AUG-1992 (Rel. 23,
01-AUG-1992 (Rel. 23,
01-FEB-1995 (Rel. 31,
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                 Ribosomal protein; Repeat.
DOMAIN 9 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 111-128 STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                           InterPro; IPR000851; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1. Biol. Chem. 266:20007-20010(1991).
1- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                       18 GLGGRG
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                                                                                                                                                     Similarity 6; Conserv
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2 X 4 AA TANDEM REPE
9 X 2 AA TANDEM REPE
W; 9092DB564AA624C9 C
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MBL outstation -
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
2-DEHYDRO-3-DEOXYGLUCONOKINASE (EC 2.7.1.45) (2-KETO-3-DEOXYGLUCONOKINASE) (3-DEOXY-2-OXO-D-GLUCONATE KINASE) (KDG KINASE).
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STRAIN=RD / KW20 / ATCC 5107;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Kerlavage K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001623; -. InterPro; IPR002939; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION:
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les 6; Conserv
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33244 MW;
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                                                                                                                                                                                                                                                                                                                       gamma subdivision;
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Pred. No.
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; 9EE75066F2340F15 CRC64;
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_HSV6U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel.
01-MAR-1992 (Rel.
01-OCT-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "whole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd}. ";
                                                                                Virology 209:29-51(1995).
-i- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL16,
HSV-6 ORFILR, EHV-1 46, HCMV UL94, EBV BGLF2, HSV 33, AND VZV 44.
                                                                                                                                                                                  Gompels U.A.,
                                                                                                                                                                                                                                                        J. Virol.
                                                                                                                                                                                                                                                                                                                                                                                             Betaherpesvirinae; Roseolovirus
                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                             Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  U65 OR 11R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P24442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Kinase. SEQUENCE 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002173;
Pfam; PF00294; pfkB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; HI0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32690; AAC21727.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.
                                                                                                                                                                    Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
                                                                                                                                                                                                    MEDLINE=95266321; PubMed=7747482;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          Barrell B.G.;
                                                                                                                                                                                                                                                                                                                         MEDLINE=90080132; PubMed=2152817;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10370;
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BETA-L-ARABINOSE 1-PHOSPHATE
                                                                                                                                "The DNA sequence of human herpesvirus-6: and genome evolution.";
                                                                                                                                                                                                                                                                                                         Lawrence G.L., Chee
                                                                                                                                                                                                                                                      'Human herpesvirus 6 is closely related to J. Virol. 64:287-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 GYLRNK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GYLRNK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Last annotation updat
                                                                                                                                                                                                                                                                                                          Craxton M.A., Gompels U.A., Honess R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                no RNA stage;
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Pred. No.
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37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                      structure,
                                                                                                                                                                                                                                                                          human cytomegalovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 314;
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                                                                                                                                                        coding content,
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                                                                                                                                                                                                                                                                                                                              Pfam; PF00361; oxidored_q1; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; SEQUENCE 348 AA; 38788 MW; DD123DADD1CF61EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
NADH-191QUINONE OXIDOREDUCTASE CHAIN 2 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y09527; CAA70717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97398704; PubMed=9254918; Delarbre C., Barriel V., Tillier S., "The main features of the craniate m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Myxinidae; Myxininae; Myxine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X83413; CAA58357.1; -.
EMBL; M68963; AAA65574.1; -.
PIR; B36769; B36769.
SEQUENCE 335 AA; 37877 MW;
                                                                                                                     163
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                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Biol. Evol. 14:807-813(1997).
CATALYTIC ACTIVITY: NADH + UBIQUINONE SUBCELLULAR LOCATION: INTEGRAL MEMBRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the COI genes were established
                                                                                                                                                                 GGFGGL 6
                                                                                                                     GGFGGL
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                                                                                                                                                                                                                Similarity 6; Conser
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                                                                                                                     168
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Pred. No.
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    355
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2 (EC 1.6
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PROTEIN. MITOCHONDRIAL
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5
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DNA between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ancestor with the
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RESULT 23
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P52424;
01-OCT-1996
                                                                                                           Vigna unguiculata (Cowpea).

Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Fabales; Fabaceae; Papilionoideae; Vigna.
                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2090 (Rel. 40, Last annotation update)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE, CHI
(EC. 6.3.3.1) (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- CATALYTIC ACTIVITY: ATP + 5'.PHOSPHORIBOSYL-FORMYLGLYCINAMIDINE
-BDP + ORTHOPHOSPHARE + 5'.PHOSPHORIBOSYL-5-AMINOIMIDAZOLE.

-!- PATHWAY: FIFTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolating the Arabidopsis thallana genes for de novo synthesis by suppression of Escherichia coli mutants. 5'-phosphoribosyl-5-aminodnidazole synthetase."; Plant Physiol. 102:387-399(1993).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         SYNTHASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE, CHLOROPLAST PRECURSO (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR
                                                                          NCBI_TaxID=3917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00586; AIRS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L12457; AAC37341.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Senecoff J.F., Meagher R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassicales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355
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Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORIBOSYLFORMYLGLYCINAMIDINE
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                                                                                                                                                            Tracheophyta; S
dicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no rest
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                                                                                                                                                            Spermatophyta;
e; eurosids I;
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in no way
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smith P.M.C., Mann A.J., Hall D.J., Atkins C.A.;
submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
submitted (JUL-1995) to ATP + 5'-PHOSPHORIBOSYL-FORMYLGLYCINAMIDINE
-!- CATALYTIC ACTIVITY: ATP + 5'-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE.
ADP + ORTHOPHOSPHATE + 5'-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE.
-!- PATHWAY: FIFTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-89235250; PubMed=2469734;
Stasiak P.C., Purkis P.E., Leigh I.M., Lane E.B.;
"Keratin 19: predicted amino acid sequence and bro
distribution suggest it evolved from keratinocyte
J. Invest. Dermatol. 92:707-716(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).
                                                                                                                                                                                                                                                                                            Stasiak P.C., Lane E.B.;
"Sequence of cDNA coding for human keratin 19.";
Nucleic Acids Res. 15:10058-10058(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988
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-!- SIMILARITY: TO OTHER AIRS FROM BACTERIA AND EUKARYOTES
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88096504; PubMed=2447559;
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                     keratin.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE FROM N.A
                                                        Proc. Natl.
                                                                                                              "Sequence of the human 40-kDa keratin reveals an unusual structure with very high sequence identity to the corresponding bovine
                                                                                                                                                                                 Eckert R.L.;
                                                                                                                                                                                                          MEDLINE=88124986; PubMed=2448790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 GGFGGL 98
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                                                            Acad. Sci.
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100.0%; Pred. No.
                                                            U.S.A. 85:1114-1118(1988)
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CHLOROPLAST (POTENTIAL).
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15D0EF11127C9EE6 CRC64;
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RESULT 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electrophoresis 13:960-969(1992).

FINCTION: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICOPIBRILLAR REPORTION: THERE ARE TWO TYPES OF CYTOSKELETAL AND II (NEUTRAL TO KERATIN: I (ACIDIC; 40-55 KDA) [K9 TO K20] AND II (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K8]; BOTH A BASIC AND AN ACIDIC KERATIN ARE REQUIRED FOR FILAMENT ASSEMBLY.

SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.

DOMAIN: THIS KERATIN DIFFERS FROM ALL OTHER IF PROTEINS IN LACKIN THE C-TERMINAL TAIL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF202321; AAF27048.1; PIR; A60779; KRHU9. SWISS-2DPAGE; P08727; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E. Vandekerckhove J.;
YFJD_ECOLI STANDARD; P37908; P76600; P76601; P77009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y00503; CAA68556.1; -. EMBL; J03607; AAA36044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein database of normal human epidermal keratinocytes.";
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Pfam; PF00038; filament;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Microsequences of 145 proteins recorded in the two-dimensional gel
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100.0%; Pred. No.
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A -> G (IN REF. 3).
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Rudd K.E.;

Rudd K.E.;

Unpublished observations (AUG-1994).

-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-: SIMILARITY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO

H.INFLUENZAE H10107.

-: CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A

FRAMESHIT IN POSITION 199 THAT PRODUCES TWO ORFS.

-: CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO NUMEROUS
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15-DEC-1998 (Rel. 37,
01-OCT-2000 (Rel. 40,
HYPOTHETICAL 46.4 KDA
YFJD OR B2612/B2613.
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SEQUENCE,
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                                                                                                                                                                   EMBL; AE000347; AAC75661.1; ALT_FRAME. EMBL; AE000347; AAC75662.1; ALT_FRAME. EMBL; D90888; BAA16497.1; ALT_INIT. EMBL; X07863; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See l or send an email to license@isb-sib.ch).
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MEDLINE-88319942; PubMed=3045760;
Lipinska B., King J., Ang D., Georgopoulos C.;
"Sequence analysis and transcriptional regulation of the Escherichia coli grpE gene, encoding a heat shock protein.";
Nucleic Acids Res. 16:7545-7562(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                               Hypothetical
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                                                                                                                                                        EcoGene; EG12442;
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                                                                                                            Pfam;
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Copyright (c) 1993 - 2000 Compugen Ltd
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hypothetical prote	C84865	N	292	9.0	0	48
probable transcrip	A83443	N	288	9.0	6	47
hypothetical prote	D84057	N	284	9.0	6	46
conserved hypothet	F75548	ν	277	9.0	6	4.5
4-amino-4-deoxycho	C82128	2	277	9.0	. 6	44
. nitrogenase (EC 1.	A61030	2	274	9.0	0	43
fibroin heavy chai	B61615	N	268	9.0	6	42
probable U1 small	T37948	N	261	9.0	6	41
т.	G69997	Ν	256	9.0	. თ	40
stationary-phase s	T09407	N	249	9.0	0	39
probable transport	G85907	N	227	9.0	· 61	ω 8
hypothetical prote	н65039	ب	227	9.0	. თ	37
hypothetical prote	T22900	N	213	9.0	. 6	36
hypothetical prote	H85747	N	203	•	6	ω 5
superinfection exc	D64885	N	203	9.0	6	34
hypothetical prote	B82471	ω	188	9.0	б	33
	B54762	2	158	9.0	6	32
hypothetical prote	H72781	N	148	9.0	6	31
ribosomal protein	S72630	ผ	140	9.0	6	30

## ALIGNMENTS

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A;Cross-references: EMBL:AF027686; NID:g2565428; PIDN:AAB82000.1; PID:g2565429
                               A; Molecule type: mRNA
A; Residues: 1-151 < JOS>
                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                             submitted to the EMBL Data Library, October 1997
A;Description: A cDNA coding for a glycine-rich protein
A;Reference number: Z16281
A;Accession: T08002
                                                                                                                                                                                                                             glycine-rich protein - common sainfoin
C;Species: Onobrychis viciifolia (common sainfoin)
C;Date: 21-May-1999 #sequence_revision 21-May-1999
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T08002
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C;Accession: B33910
R;Reuter, D.; Schuh, R.; Jaeckle, H.
R;Reitersen Spalt (sal) evolved during Drosophila speciation A;Reference number: A33910; MUID:89315821
A;Accession: B33910
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A;Molecule type: DNA
A;Residues: 1-139 <REU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Drosophila simulans
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sal homeotic protein - fruit fly (Drosophila simulans)
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987 A;Accession: F70726 A;Accession: F70726 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin; K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical glycine-rich protein Rv1450c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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E70917
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                          C;Genetics:
A;Gene: Rv1450c
C;Superfamily:
                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1329 <COL> A;Cross references: GB:295844; GB:AL123456; NID:g3250713; PIDN:CAB09271.1; PID:g2131046 A;Experimental source: strain H37Rv A;Experimental source:
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C; Superfamily: Phaseolus glycine-rich cell wall protein 1.8
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                                                                                                                                                                                                                                                                                                                                                            A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: E70917
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8; Conser
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                          C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S16815; S48418
R;Smith, V; Barrell, B.G.
EMBO J. 10, 2627-2634, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T23158
                                                                                                                                      SNP1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate_names: protein YILO61c
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        A; Title: Cloning of a yeast U1 snRNP
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hypothetical protein F13I12.120 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000 C;Accession: T45643
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A; Residues: 1-100 <CHO>
A; Cross-references: EMBL: AL133292
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-cct-1999 #sequence_revision 15-oct-1999 #text_change 21-Jan-2000
C;Accession: T23158
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A; Accession: T45643
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submitted to the Protein
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A;Introns: 89/3; 104/3; 126/3
C;Superfamily: Phaseolus glycine-rich cell wall
                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-284 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, January 1996
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259 GGFGGLG
                                                                           Local Similarity hes 7; Conser
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    265
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100.0%; Pred. No.
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o. 7.5;
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70K protein homologue:

functional conservation

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L-iditol 2-dehydrogenase (EC 1.1.1.14) - fission yeast (Schizosaccharomyces pombe) R;Alternate names: sorbitol dehydrogenase C;Species: Schizosaccharomyces pombe) C;Date: 13-Jan-1995 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Accession: T39670; S38345; S35981 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Borzym, K.; Klages, S.; Langer, M.; Rajandream, M.A.; Barrell, R.; Rajandream, M.; Raja
               A; Reference number: Z21847
A; Accession: T39670
                                                                      submitted to the EMBL Data Library, November 1998

A:Paference number 1998
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J. Mol. Biol. 285, 149-161, 1999
A;Title: Novel organization and sequences of five genes encoding all six enzymes for de A;Reference number: Z20841; MUID:99096912
A;Accession: T30523
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C; Superfamily: dihydroorotate oxidase
C; Keywords: oxidoreductase
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A; Residues: 1-314 <GAO>
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C;Superfamily: yeast SNP1 protein; ribonucleoprotein repeat
C;Keywords: nucleus
F;108-178/Domain: ribonucleoprotein repeat homology <RRM2>
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A;Residues: 1-300 <SM2>
A;Cross-references: GB:Z47047; EMBL:Z38060; NID:g603997; PID:g763285; GSPDB:GN00009; MIF
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A;Experimental source: strain AB972
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Residues: 1-300 <SMI>
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Pred. No.
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o. 7.8;
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probable dnaJ2 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: D70587
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S72599
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A;Start codon: GTG C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology F;4-68/Domain: dnaJ amino-terminal homology <DNJ>
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C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-378 <SMI>
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A; Accession: S72599
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C; Complex: homotetramer
C; Function:
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A;Molecule type: DNA
A;Residues: 14-360 <WAZ>
A;Cross-references: EMBL:X74422; NID:g396478; PIDN:CAA52443.1; PID:g396479
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A;Accession: S38345
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Eur. J. Biochem. 217, 731-736, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: SPDB: SPBC1773.05c; tms1
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A; Residues: 1-360 <LYN>
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                                                                                                                                             Query Match
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Best Local :
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82 GGFGGLG 88
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                                              1 GGFGGLG 7
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tes 7; Conserv
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                                                                                                                        100.0%;
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100.0%; Pred. No.
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5 N
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GTP-binding protein Obg - Deinococcus radiodurans (strain R1)
GTSpecies: Deinococcus radiodurans
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence-revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: B75563
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.; White, O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R
A;Reference number: A75250; MUID:20036896
A;Accession: B75563
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C;Superfamily: heat shock protein dnaJ; dnaJ amin
F;4-68/Domain: dnaJ amino-terminal homology <DNJ>
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A; Residues: 1-382 <COL>
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                                                                                                                 C; Date: 26-Feb-1997
C; Accession: S73419
                                                                                                                                            C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
                                                                                                                                                                                                                         signal recognition particle protein ffh - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: hypothetical protein D09_orf450
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C;Superfamily: GTP-binding protein obg; translation elongation factor Tu homology
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A;Residues: 1-438 <WHI>
A;Cross-references: GB:AE001871; GB:AE000513; NID:g6457740; PIDN:AAF09676.1; PID:g645774
A;Experimental source: strain R1
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniag A;Reference number: S73327; MUID:97105885
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nes 7; Conser
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-450 <HIM>
A;Rosidues: 1-450 <HIM>
A;Cross-references: EMBL:AE000011; GB:U00089; NID:g1673740; PIDN:AAB95741.1; PID:g167
A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIFLASEL, C.M.; NOTRIS, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, i rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A; Reference number: A71250: MHTD-QR333770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable preprotein translocase subunit (secY) - syphilis spirochete C;Speckes: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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C; Superfamily: signal recognition particle 54K protein
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           A;Cross-references: GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98325.1; PID:e24855
A;Experimental source: Strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                               probable dinX protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: F70760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A71250; MUID: 98332770 A; Accession: F71351
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                                                                                                                                                                                                       A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
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C; Superfamily:
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A;Experimental source: strain Nichols
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A; Residues: 1-450 <COL>
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                                                                                                                                                                                                                                                                                             Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
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100.0%; Pred. No.
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100.0%; Pred. No. 11
tive 0; Mismatches
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A:Cross-references: EMBL:X75015; NID:g453154; PIDN:CAA52924.1; PID:g453155
R;Langbein, L.; Heid, H.W.; Moll, I.; Franke, W.W.
Differentiation 55, 57-71, 1993
A:Title: Molecular characterization of the body site-specific human epidermal cytokerati
A:Reference number: I37943; MUID:94131202
                                                                                                                                                                                                                                                                                                                                                                                                  keratin 9, type I, cytoskeletal - human
N;Alternate names: cytokeratin 9; scatter protein 60K chain, placental
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Oct-1999
C;Accession: I37984; S40307; S77921; S41161; B35494; I37943
R;Reis, A.; Henniaes, H.C.; Langbein, L.; Digweed, M.; Mischke, D.; Drechsler, M.; Schrod Nature Genet. 6, 174-179, 1994
A;Title: Keratin 9 gene mutations in epidermolytic palmoplantar keratoderma (EPPK).
A;Reference number: I37984; MUID:94214498
A;Accession: I37984
A;Molecule type: protein
A;Residues: 29-53;62-104;167-188;199-233;241-249;295-362;374-430;450-480;579-604 <LAF>
                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-622 <LAN>
                                                                                               A;Cross-references: EMBL:Z29074; NID:g435475; PIDN:CAA82315.1;
                                                                                  A; Accession: S77921
                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-622 < RES>
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A; Cross-references: GB:AE000790; NID:92690224; PIDN:AAC66282.1;
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein BBA50 - Lyme disease spirochete plasmid A/lp54 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
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                                                                                                    PID:g435476
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hypothetical protein T17H7.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28899
R;Favello, A.
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Best Local Similarity
7; Conserv
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
C;Keywords: isomerase
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A;Map position: 17q12-17q21
A;Introns: 213/3; 241/2; 293/3; 347/3; 389/3; 464/2
A;Note: defects in this gene may cause epidermolytic |
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; intermediate filament
F;1-153/Domain: heal #status predicted <HEA>
F;154-459/Domain: tail #status predicted <ROD>
F;460-622/Domain: tail #status predicted <TAI>
                                                                                                                      T28899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16157.1; PID:g3128305
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-652 <VLC>
                                                                                                                                            RESULT 19
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A; Accession: T03504
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A;Tille: Sequence of a 189-kb segment of the chromosome of Rhodobacter caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: DNA gyrase chain b C;Species: Rhodobacter capsulatus
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A;Residues: 1-11./SR',13-622 <LAW>
A;Residues: 1-11./SR',13-622 <LAW>
A;Residues: 1-11./SR',13-622 <LAW>
A;COOST-references: EMBL:Z29074; NID:g435475; PIDN:CAA82315.1; PID:g435476
R;Rosen, E.M.; Meromsky, L.; Romero, R.; Setter, E.; Goldberg, I.
Biochem. Biophys. Res. Commun. 168, 1082-1088, 1990
A;Title: Human placenta contains an epithelial scatter protein.
A;Reference number: A35494; MUID:90267446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 'X', 450-465 < ROS>
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A; Reference number: S41161
A; Accession: S41161
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R.Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, F. rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T. they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770
A;Accession: F71340
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A; Description: The sequence of C. elegans cosmid T17H7.
A; Reference number: Z20540
A; Accession: T28899
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: F71340
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A;Molecule type: DNA
A;Residues: 1-682 <FAV>
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Colecule type
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A; Introns: 85/3; 147/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable tpr protein J (tprJ) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: F71301
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A; Residues: 1-756 <COL>
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Local Similarity 100.0%; Pred. No. 17
hes 7; Conservative 0; Mismatches
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100.0%; Pred. No.
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C;Accession: C71340

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable alpha-mannosidase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE001211; GB:AE000520; NID:g3322582; PIDN:AAC65300.1; PID:g332A;Experimental source: strain Nichols
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                                                                                                                                                                                                                                                                                                         M.; Ohfukū, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: G71133
A;Accession: G71133
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A; Residues: 1-762 <COL>
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                                                                                                                                                             A; Note: this accession replaces an interim accession
                                                                                                                                                                                                              A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29929.1; PID:d1030872; PID:g32
                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-856 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                        R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: G71133
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                                                                                                                                                                                       A; Experimental source: strain OT3
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R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Recession: H96597
A; Accession: H96597
A; Accession: H96597
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Thes 7; Conserve
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A; Gene: T5A14.5
Job time: 44 sec
                                   Search completed: July 12, 2001, 06:17:29
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A; Introns: 12/3; 48/3; 258/3; 327/3; 643/1; 916/2
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A;Experimental source: strain Bristol N2; clone F26G5
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